(b) cultivating the cells under a selection pressure;

(c) selecting or screening for one or more transformants expressing a desired characteristic; and

(d) isolating the transformant(s) of interest.

3. (Amended) The method of claim 1, wherein the polynucleotide sequence further comprises a control sequences.

4. (Amended.) The method according to claim 1, wherein the polynucleotide sequence of interest encodes a hormone, an enzyme, a receptor or a portion thereof, an antibody or a portion thereof, or a reporter, or a regulatory protein.

7. (Amended) The method according to claim 3, wherein the control sequence is an enhancer sequence, a leader sequence, a polyadenylation sequence, a propeptide sequence, a promoter, a replication initiation sequence, a signal sequence, a transcriptional terminator or a translational terminator.

9. (Amended) The method according to claim 1, wherein the selection marker polynucleotide sequence is selected from the group of genes which encode a product which is responsible for one of the following: resistance to biocide or viral toxicity, resistance to heavy metal toxicity, prototrophy to auxotrophs.

11. (Amended.) The method of claim 9, wherein the selection marker polynucleotide sequence is a gene selected from the group consisting of *argB* (ornithine carbamoyltransferase), *amdS* (acetamidase), *bar* (phos-hinothricin acetyltransferase), *hemA* (5-aminolevulinate synthase), *hemB* (porphobilinogen synthase), *hygB* (hygromycin phosphotransferase), *niaD* (nitrate reductase), *prn* (proline permease), *pyrG* (orotidine-5'-phosphate decarboxylase), *pyroA*, *riboB*, *sC* (sulfate adenyltransferase), and *trpC* (anthranilate synthase).

12. (Amended) The method of claim 1, wherein the replication initiating sequence is a nucleic

acid sequence selected from the group consisting of:

(a) a replication initiating sequence having at least 80% identity with the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, as determined using the GAP computer program with a GAP creation penalty of 5.0 and GAP extension penalty of 0.3, and is capable of initiating replication; and

(b) a replication initiating sequence which hybridises under low stringency conditions with (i) the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, or (ii) the respective complementary strands, wherein the low stringency conditions are defined by prehybridization and hybridization at 42°C in 5x SSPE, 0.3% SDS, 200 mg/ml sheared and denatured salmon sperm DNA, and 25% formamide, and wash conditions are defined at 50°C for 30 minutes in 2x SSC, 0.2% SDS.

13. (Amended) The method of claim 12, wherein the nucleic acid sequence has at least 80% identity with the nucleic acid sequence of SEQ ID NO:1 or SEQ ID NO:2, as determined using the GAP computer program with a GAP creation penalty of 5.0 and GAP extension penalty of 0.3.

14. (Amended.) The method of claim 12, wherein the replication initiating polynucleotide sequence is obtained from a filamentous fungal cell.

17. (Twice amended.) The method of claim 12, wherein the replication initiating polynucleotide sequence has the nucleic acid sequence set forth in SEQ ID NO:1 or SEQ ID NO:2.

18. (Amended.) The method of claim 2, wherein the polynucleotide sequence of interest was created by mutagenesis, by random mutagenesis, by use of a physical or chemical mutagenizing agent, by use of a doped oligonucleotide, by DNA shuffling, by subjecting the nucleic acid sequence to PCR generated mutagenesis, or by use of any combination thereof.

Please add new claim 30, as follows:

30. (New.) The method of claim 1, wherein the polynucleotide sequence of interest is a control

B'11 Cont'd

sequences.